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AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of the claims in the application.

1. -2. (*Canceled*)

3. (*Currently amended*) A method in a computer system for ~~displaying data on~~ generating a graphic display for visualization of gene expression in a molecular topography, comprising:

providing a first set of data, the data comprising gene expression measurements and descriptive information for a first plurality of polynucleotides;

defining an X-Y plane having a first axis corresponding to sequence identifiers and a second axis corresponding to polynucleotide sizes;

(a) generating a first gene expression profile within the X-Y plane for the first of a plurality of gene expression indicating polynucleotides including for each of the polynucleotides, the first profile comprising a plurality of peaks with each peak corresponding to a polynucleotide, the peak defined by:

(i) a first value for a first polynucleotide characteristic comprising a sequence identifier for the polynucleotide;

(ii) a second value for a second polynucleotide characteristic different from said first characteristic comprising a measure of size of the polynucleotide, wherein an intersection between the first value and the second value defines a point within the X-Y plane; and

(iii) at the point, plotting along a Z-axis intersecting the X-Y plane a third value that is a measure of the quantity of the polynucleotide;

(b) ~~calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and~~

(c) ~~displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby wherein the plurality of~~

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peaks is generated for the first plurality of polynucleotides so that the graphic display comprises a molecular topography of gene expression.

4.-24. (*Canceled*)

25. (*New*) The method of claim 3, further comprising:
providing a second set of data comprising gene expression measurements and descriptive information for a second plurality of polynucleotides;
generating a second gene expression profile within the X-Y plane for the second plurality of polynucleotides;
comparing the first and second gene expression profiles to generate a differential gene expression profile;
wherein the graphic display comprises the molecular topography of differential gene expression.

26. (*New*) The method of claim 25, wherein one of the first and second sets of data corresponds to a reference sample and the other of the first and second sets of data corresponds to a test sample.

27. (*New*) The method of claim 26, wherein the differential gene expression is diagnostic of a condition or disease.

28. (*New*) The method of claim 3, further comprising:
providing a plurality of subsequent sets of data for the same or comparable sample as the first set of data in a temporal succession; and
generating and displaying gene expression profiles for each subsequent set of data to observe dynamic changes in gene expression over time.

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29. (*New*) The method of claim 28, wherein the subsequent sets of data are taken from samples comprising cells undergoing one or more of growth, differentiation and division.

30. (*New*) The method of claim 28, wherein the subsequent sets of data are taken from samples comprising cells undergoing disease process and/or therapy.

31. (*New*) The method of claim 25, further comprising:
providing a plurality of subsequent sets of data for the same or comparable sample as the first and second sets of data in a temporal succession; and
generating and displaying differential gene expression profiles for each subsequent set of data to observe dynamic changes in differential gene expression over time.

32. (*New*) The method of claim 31, wherein the subsequent sets of data are taken from samples comprising cells undergoing one or more of growth, differentiation and division.

33. (*New*) The method of claim 31, wherein the subsequent sets of data are taken from samples comprising cells undergoing disease process and/or therapy.

34. (*New*) A method in a computer system for generating a graphic display for visualization of gene expression data, comprising:
providing a first set of data, the data comprising gene expression measurements and descriptive information for a first plurality of polynucleotides;
defining an X-Y plane having a first axis corresponding to sequence identifiers and a second axis corresponding to polynucleotide sizes;
plotting within the X-Y plane a plurality of points corresponding to the first plurality of polynucleotides according to their sequence identifiers and polynucleotide sizes; and
for each point within the plane, plotting along a Z-axis intersecting the X-Y plane a measured value corresponding to a quantity of mRNA produced for the polynucleotide plotted at the point so that a peak extending from the X-Y plane is generated;

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wherein the graphic display comprises a three-dimensional plot representative of gene expression for the first plurality of polynucleotides.

35. (*New*) The method of claim 34, further comprising:
providing a second set of data comprising gene expression measurements and descriptive information for a second plurality of polynucleotides;
generating a second gene expression profile within the X-Y plane for the second plurality of polynucleotides;
comparing the first and second gene expression profiles to generate a differential gene expression profile;
wherein the graphic display comprises the molecular topography of differential gene expression.

36. (*New*) The method of claim 35, wherein one of the first and second sets of data corresponds to a reference sample and the other of the first and second sets of data corresponds to a test sample.

37. (*New*) The method of claim 36, wherein the differential gene expression is diagnostic of a condition or disease.

38. (*New*) The method of claim 32, further comprising:
providing a plurality of subsequent sets of data for the same or comparable sample as the first set of data in a temporal succession; and
generating and displaying gene expression profiles for each subsequent set of data to observe dynamic changes in gene expression over time.

39. (*New*) The method of claim 38, wherein the subsequent sets of data are taken from samples comprising cells undergoing one or more of growth, differentiation and division.

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40. (*New*) The method of claim 38, wherein the subsequent sets of data are taken from samples comprising cells undergoing disease process.

41. (*New*) The method of claim 35, further comprising:
providing a plurality of subsequent sets of data for the same or comparable sample as the first and second sets of data in a temporal succession; and
generating and displaying differential gene expression profiles for each subsequent set of data to observe dynamic changes in differential gene expression over time.

42. (*New*) The method of claim 41, wherein the subsequent sets of data are taken from samples comprising cells undergoing one or more of growth, differentiation and division.

43. (*New*) The method of claim 41, wherein the subsequent sets of data are taken from samples comprising cells undergoing disease process and/or therapy.